specifically recognizes the 5' flanking region in SEQ ID No. 8 or the 3' flanking region in SEQ ID No. 10 of MS-B2.

24. (Twice Amended) The method of claim 23, said method comprising amplifying a DNA fragment of between 160 and 200 bp from a nucleic acid present in said transgenic *Brassica* plant, or cell or tissue thereof, or trangenic *Brassica* plant material, using a polymerase chain reaction with at least two primers, one of which recognizes the 5' flanking region in SEQ ID No. 8 or 3' flanking region in SEQ ID No. 10 of MS-B2, the other which recognizes a sequence within the foreign DNA.

33. (Amended) A method for confirming seed purity, which method comprises detecting an MS-B2 specific region comprising the insertion site of MS-B2 with a specific primer or probe which specifically hybridizes to the 5' flanking region of SEQ ID No. 8 or the 3' flanking region of SEQ ID No. 10 of MS-B2, and thus confirming seed purity if the MS-B2 specific DNA is so detected in seed samples.

34. (Amended) A method for screening seeds for the presence of MS-B2, which method comprises detecting an MS-B2 specific region comprising the insertion site of MS-B2 with a specific primer or probe which specifically hybridizes to the 5' flanking region of SEQ ID No. 8 or the 3' flanking region of SEQ ID No. 10 of MS-B2, and thus confirming the presence of MS-B2 if the MS-B2 specific DNA sequence is so detected in samples of seed lots.

Please add the following claims:

--35. (New) A method for confirming seed purity, which method comprises not detecting an MS-B2 specific DNA sequence using a specific primer or probe which specifically hybridizes to the 5' flanking region of SEQ ID No. 8 or the 3' flanking region of SEQ ID No. 10 of MS-B2, and thus confirming seed purity, if the MS-B2 specific DNA is not so detected.

36. (New) A method for identifying a *Brassica* plant, or cell or tissue thereof, or *Brassica* plant material not comprising elite event MS-B2, which method comprises establishing whether a DNA fragment of between 160 and 200 base pairs cannot be amplified from the genomic DNA of the plant, cell, tissue or plant material, using a polymerase chain reaction with at least two primers, one of which recognizes the 5' flanking region of SEQ ID No. 8 or the 3' flanking region of SEQ ID No. 10 of MS-B2, another of which recognizes a sequence within foreign DNA, which method amplifies a DNA fragment of between 160 and 200 base pairs from DNA comprising elite event MS-B2.--